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 NEWS  2          "Ask CAS" for self-help around the clock
 NEWS  3  FEB 25  CA/CAPLUS - Russian Agency for Patents and Trademarks
                  (ROSPATENT) added to list of core patent offices covered
 NEWS  4  FEB 28  PATDPAFULL - New display fields provide for legal status
                  data from INPADOC
 NEWS  5  FEB 28  BABS - Current-awareness alerts (SDIs) available
 NEWS  6  FEB 28  MEDLINE/LMEDLINE reloaded
 NEWS  7  MAR 02  GBFULL: New full-text patent database on STN
 NEWS  8  MAR 03  REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS  9  MAR 03  MEDLINE file segment of TOXCENTER reloaded
 NEWS  10 MAR 22  KOREAPAT now updated monthly; patent information enhanced
 NEWS  11 MAR 22  Original IDE display format returns to REGISTRY/ZREGISTRY
 NEWS  12 MAR 22  PATDPASPC - New patent database available
 NEWS  13 MAR 22  REGISTRY/ZREGISTRY enhanced with experimental property tags

 NEWS EXPRESS  JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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=> File Medline EMBASE Biosis CAplus
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                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

FILE 'MEDLINE' ENTERED AT 18:07:17 ON 25 MAR 2005

FILE 'EMBASE' ENTERED AT 18:07:17 ON 25 MAR 2005
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number of left parentheses.

=>  s (human or sapiens) (2A) (myoD)
   3 FILES SEARCHED...
L1          108 (HUMAN OR SAPIENS) (2A) (MYOD)

=> s l1 (8A) ((fusion protein) or tag)
L2            0 L1 (8A) ((FUSION PROTEIN) OR TAG)

=> s (cdk4 binding protein)
L3           19 (CDK4 BINDING PROTEIN)

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ENTER L# LIST OR (END):l3
DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L3
L4             7 DUPLICATE REMOVE L3 (12 DUPLICATES REMOVED)

=> d l4 1-7 bib ab

L4   ANSWER 1 OF 7  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 1
AN   2004:392230  BIOSIS
DN   PREV200400390794
TI   A study of interacting proteins with hASB-8.
AU   Chen Fu-song [Reprint Author]; Lu Hong; Li Yu-yang
CS   Sch Life SciInst GenetState Key Lab Genet Engn, Fudan Univ, Shanghai,
     200433, China
     honglv@fudan.edu.cn
SO   Fudan Xuebao Zirankexueban, (April 2004) Vol. 43, No. 2, pp. 141-146.
     print.
     ISSN: 0427-7104 (ISSN print).
DT   Article
LA   Chinese
OS   DDBJ-AF398969; EMBL-AF398969; GenBank-AF398969; DDBJ-AF464877;
     EMBL-AF464877; GenBank-AF464877; DDBJ-NM005648; EMBL-NM005648;
     GenBank-NM005648; DDBJ-NM013376; EMBL-NM013376; GenBank-NM013376
ED   Entered STN: 6 Oct 2004
     Last Updated on STN: 6 Oct 2004
AB   hASB-8 is a human novel gene that has apparent effects on the growth of
     tumor cells.  It is a new member of human ASB protein family, with a 96%
     homology to mouse ASB-8 protein.  Conserved domain analysis indicated that
     it contained four Ankyrin repeats in its N terminal and one SOCS box in
     its C terminal.  By using the yeast two-hybrid technology, a human
     placenta cDNA library was screened and 2 positive clones named Elongin C
     and CDK4 binding protein were obtained.
     Their interaction with hASB-8 was also tested in diploid yeasts.  These
     results indicated that hASB-8 may mediate the interaction between target
     proteins and ubiquitination complex, and correlate with the transcription
     process of target genes in tumor cells.
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L4 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:362984 CAPLUS
DN 141:83922
TI Differentiation of DNA reactive and non-reactive genotoxic mechanisms using gene expression profile analysis
AU Dickinson, Donna A.; Warnes, Gregory R.; Quievryn, George; Messer, Joseph; Zhitkovich, Anatoly; Rubitski, Elizabeth; Aubrecht, Jiri
CS Pfizer Global Research and Development, Groton, CT, 06340, USA
SO Mutation Research (2004), 549(1-2), 29-41
CODEN: MUREAV; ISSN: 0027-5107
PB Elsevier Science B.V.
DT Journal
LA English
AB Genotoxic stress triggers a variety of biol. responses including the transcriptional activation of genes regulating DNA repair, cell survival and cell death. Here, the authors investigated whether gene expression profiles can differentiate between DNA reactive and DNA non-reactive mechanisms of genotoxicity. The authors analyzed gene expression profiles and micronucleus levels in L5178Y cells treated with cisplatin and sodium chloride. The assessment of cisplatin genotoxicity (up to six-fold increase in the number of micronuclei) and gene expression profile (increased expression of genotoxic stress-associated genes) was in agreement with cisplatin mode of action as a DNA adduct-forming agent. The gene expression profile anal. of cisplatin-treated cells identified a number of genes with robust up regulation of mRNA expression including genes associated with DNA damage (i.e., members of GADD45 family), early response (i.e., cFOS), and heat shock protein (i.e., HSP40 homolog). The gene expression changes correlated well with DNA damage as measured by DNA-protein crosslinks and platinum-DNA binding. To differentiate the genotoxic stress-associated expression profile of cisplatin from a general toxic stress, the authors have compared the gene expression profile of cisplatin-treated cells to cells treated with sodium chloride, which causes osmotic shock and cell lysis. Although the sodium chloride treatment caused a two-fold induction of micronuclei, the gene expression profile at equitoxic concns. was remarkably distinct from the profile observed with cisplatin. The profile of sodium chloride featured a complete lack of expression changes in genes associated with DNA damage and repair. In summary, the gene expression profiles clearly distinguished between DNA reactive and non-reactive genotoxic mechanisms of cisplatin and sodium chloride. The authors' results suggest the potential utility of gene expression profile anal. for elucidating mechanism of action of genotoxic agents.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 7 MEDLINE on STN DUPLICATE 2
AN 2003215067 MEDLINE
DN PubMed ID: 12736710
TI Regulation of CREB-mediated transcription by association of **CDK4 binding protein** p34SEI-1 with CBP.
AU Hirose Takuji; Fujii Ryouji; Nakamura Hiroshi; Aratani Satoko; Fujita Hidetoshi; Nakazawa Minako; Nakamura Kohzo; Nishioka Kusuki; Nakajima Toshihiro
CS Department of Genome Science, Institute of Medical Science, St. Marianna University School of Medicine, Kawasaki 216-8512, Japan.
SO International journal of molecular medicine, (2003 Jun) 11 (6) 705-12.
Journal code: 9810955. ISSN: 1107-3756.
CY Greece
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200402
ED Entered STN: 20030509

Last Updated on STN: 20040302
Entered Medline: 20040226

AB CREB binding protein (CBP) plays a central role in cell differentiation and proliferation, interacting with a large number of nuclear factors. To find novel nuclear factors associating with CBP, we have carried out yeast two-hybrid screening of human chondrocyte cDNA library using the C/H3 region of CBP as a bait and cloned **CDK4 binding protein** p34SEI-1, the recently found cell cycle regulator. The association of p34SEI-1 with CBP was confirmed in vitro by GST pull-down assay and in vivo by coimmunoprecipitation. Results of the immunofluorescence assay also supported the association of p34SEI-1 and CBP. In reporter assay using CRE promoter, p34SEI-1 strongly suppressed CREB-mediated transcription, and this suppression was overcome by excess amount of CBP, but not by CBPDeltaCH3. It is suggested that the association of p34SEI-1 and CBP is not only involved in cell cycle regulation by CBP, but also have some effect on other CBP-dependent transcription.

L4 ANSWER 4 OF 7 MEDLINE on STN DUPLICATE 3
AN 2002683818 MEDLINE
DN PubMed ID: 12444543
TI Activation of cyclin D1-kinase in murine fibroblasts lacking both p21(Cip1) and p27(Kip1).
AU Sugimoto Masataka; Martin Nicholas; Wilks Deepti P; Tamai Katsuyuki; Huot Thomas J G; Pantoja Cristina; Okumura Ko; Serrano Manuel; Hara Eiji
CS Cancer Research UK, Paterson Institute for Cancer Research, Christie Hospital NHS Trust, Manchester M20 4BX, UK.
SO Oncogene, (2002 Nov 21) 21 (53) 8067-74.
Journal code: 8711562. ISSN: 0950-9232.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200212
ED Entered STN: 20021123
Last Updated on STN: 20021227
Entered Medline: 20021223

AB Deregulation of D-type cyclin-dependent kinases (CDK4 and 6) is widely observed in various human cancers, illustrating their importance in cell cycle control. Like other cyclin-dependent kinases (CDKs), assembly with cyclins is the most critical step for activation of CDK4/6. As previously reported elsewhere, we observed that the level of cyclinD1-CDK4 complex and its associated kinase activity were significantly low in asynchronously proliferating mouse embryo fibroblasts lacking both p21(Cip1) and p27(Kip1) (p21/p27-null MEFs). These evidences imply that p21(Cip1) and p27(Kip1) CDK inhibitors are 'essential activators' of cyclin D-kinases. We, however, discovered here that both the assembly and activation of cyclin D1-CDK4 complex occur when quiescent p21/p27-null MEFs were stimulated to re-enter the cell cycle. This mitogen-induced cyclin D1-kinase activity was blocked by overexpression of p16(INK4a) and resulted in the inhibition of S phase entry in p21/p27-null MEFs. Furthermore, ectopic expression of p34(SEI-1), a mitogen-induced **CDK4 binding protein**, increased the levels of active cyclinD1-CDK4 complex in asynchronously proliferating p21/p27-null MEFs. Together, our results suggest that there are several independent ways to stimulate the assembly of cyclin D1-CDK4 kinases. Although p21(Cip1) and p27(Kip1) play a role in this process, our results demonstrate that additional mechanisms must occur in G0 to S phase transition.

L4 ANSWER 5 OF 7 MEDLINE on STN DUPLICATE 4
AN 2001272340 MEDLINE
DN PubMed ID: 11331592
TI TRIP-Br: a novel family of PHD zinc finger- and bromodomain-interacting

proteins that regulate the transcriptional activity of E2F-1/DP-1.
AU Hsu S I; Yang C M; Sim K G; Hentschel D M; O'Leary E; Bonventre J V
CS Renal Unit, Department of Medicine, Massachusetts General Hospital and Harvard Medical School, Charlestown, MA 02129, USA.
NC DK39773 (NIDDK)
T32 DK07540 (NIDDK)
SO EMBO journal, (2001 May 1) 20 (9) 2273-85.
Journal code: 8208664. ISSN: 0261-4189.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF366400; GENBANK-AF366401; GENBANK-AF366402; GENBANK-AF366403
EM 200105
ED Entered STN: 20010604
Last Updated on STN: 20010604
Entered Medline: 20010531
AB We report the isolation of TRIP-Br1, a transcriptional regulator that interacts with the PHD-bromodomain of co-repressors of Kruppel-associated box (KRAB)-mediated repression, KRIP-1(TIF1beta) and TIF1alpha, as well as the co-activator/adaptor p300/CBP. TRIP-Br1 and the related protein TRIP-Br2 possess transactivation domains. Like MDM2, which has a homologous transactivation domain, TRIP-Br proteins functionally contact DP-1, stimulating E2F-1/DP-1 transcriptional activity. KRIP-1 potentiates TRIP-Br protein co-activation of E2F-1/DP-1. TRIP-Br1 is a component of a multiprotein complex containing E2F-1 and DP-1. Co-expression of the retinoblastoma gene product (RB) abolishes baseline E2F-1/DP-1 transcriptional activity as well as TRIP-Br/KRIP-1 co-activation, both of which are restored by the adenovirus E1A oncoprotein. These features suggest that TRIP-Br proteins function at E2F-responsive promoters to integrate signals provided by PHD- and/or bromodomain- containing transcription factors. TRIP-Br1 is identical to the cyclin-dependent kinase 4 **(cdk4)-binding protein** p34(SEI-1), which renders the activity of cyclin D/cdk4 resistant to the inhibitory effect of p16(INK4a) during late G(1). TRIP-Br1(p34(SEI-1)) is differentially overexpressed during the G(1) and S phases of the cell cycle, consistent with a dual role for TRIP-Br1(p34(SEI-1)) in the regulation of cell cycle progression through sequential effects on the transcriptional activity of E2F-responsive promoters during G(1) and S phases.

L4 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 5
AN 2000047903 MEDLINE
DN PubMed ID: 10580009
TI Regulation of CDK4 activity by a novel **CDK4-binding protein**, p34(SEI-1).
AU Sugimoto M; Nakamura T; Ohtani N; Hampson L; Hampson I N; Shimamoto A; Furuichi Y; Okumura K; Niwa S; Taya Y; Hara E
CS Paterson Institute for Cancer Research, Christie Hospital National Health Service Trust, Manchester, M20 4BX, UK.
SO Genes & development, (1999 Nov 15) 13 (22) 3027-33.
Journal code: 8711660. ISSN: 0890-9369.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF117959
EM 200001
ED Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 20000106
AB The p16(INK4a) tumor suppressor inhibits cyclin-dependent kinases (CDK4 and CDK6). Here we report the isolation of a novel gene, SEI-1, whose product (p34(SEI-1)) appears to antagonize the function of p16(INK4a).

Addition of p34(SEI-1) to cyclin D1-CDK4 renders the complex resistant to inhibition by p16(INK4a). Expression of SEI-1 is rapidly induced on addition of serum to quiescent fibroblasts, and ectopic expression of p34(SEI-1) enables fibroblasts to proliferate even in low serum concentrations. p34(SEI-1) seems to act as a growth factor sensor and may facilitate the formation and activation of cyclin D-CDK complexes in the face of inhibitory levels of INK4 proteins.

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L4   ANSWER 7 OF 7  CAPLUS  COPYRIGHT 2005 ACS on STN
AN   1996:134123  CAPLUS
DN   124:195977
TI   Cdk4 binding proteins of mammal, gene
     cloning, and use in disease diagnosis and treatment
IN   Draetta, Giulio; Gyuris, Jeno
PA   Mitotix, Inc., USA
SO   PCT Int. Appl., 114 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
     ---------------     ----   --------    --------------------   --------
PI   WO 9533819           A2    19951214    WO 1995-US7113         19950602
     WO 9533819           A3    19960321
         W:  AU, CA, JP, KR
         RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
     US 5691147           A     19971125    US 1994-253155         19940602
     AU 9526627           A1    19960104    AU 1995-26627          19950602
PRAI US 1994-253155       A     19940602
     WO 1995-US7113       W     19950602
AB   The present invention relates to the discovery of novel proteins of
     mammalian origin which can associate with the human cyclin dependent kinase 4
     (CDK4). Plasmids for producing recombinant Cdk4-binding
     protein are described. Sequences of Cdk4-
     binding proteins and genes are shown, and their use as
     anti-proliferative agents is discussed. Also, mutation and genetic
     rearrangement, as well as mRNA splicing variants are suggested as methods
     to provide further Cdk4-binding protein
     variations.


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 NEWS 10  MAR 22  KOREAPAT now updated monthly; patent information enhanced
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 NEWS 13  MAR 22  REGISTRY/ZREGISTRY enhanced with experimental property tags

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               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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                                                           ENTRY   SESSION
FULL ESTIMATED COST                                         0.21      0.21

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FILE 'EMBASE' ENTERED AT 18:45:58 ON 25 MAR 2005
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=> s (cdk4 (w) binding (w) protein)
L1            19 (CDK4 (W) BINDING (W) PROTEIN)

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The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l1 and (bHLH or (helix (w) loop (w) helix))
L2             0 L1 AND (BHLH OR (HELIX (W) LOOP (W) HELIX))
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Myc-type, 'helix-loop-helix' domain profile

PROSITE cross-reference(s)

PS50888; HLH	**Graphical PROSITE domain view of Swiss-Prot/TrEMBL hits to PS50888** **Retrieve an alignment of Swiss-Prot true positive hits:** [Clustal format, color, condensed view] [Clustal format, color] [Clustal format, plain text] [Fasta format] **Retrieve a list of all Swiss-Prot/TrEMBL entries matching PS50888**

Documentation

A number of eukaryotic proteins, which probably are sequence specific DNA-binding proteins that act as transcription factors, share a conserved domain of 40 to 50 amino acid residues. It has been proposed [1] that this domain is formed of two amphipathic helices joined by a variable length linker region that could form a loop. This 'helix-loop-helix' (HLH) domain mediates protein dimerization and has been found in the proteins listed below [2,3,E1,E2]. Most of these proteins have an extra basic region of about 15 amino acid residues that is adjacent to the HLH domain and specifically binds to DNA. They are refered as basic helix-loop-helix proteins (bHLH), and are classified in two groups: class A (ubiquitous) and class B (tissue-specific). Members of the bHLH family bind variations on the core sequence 'CANNTG', also refered to as the E-box motif. The homo- or heterodimerization mediated by the HLH domain is independent of, but necessary for DNA binding, as two basic regions are required for DNA binding activity. The HLH proteins lacking the basic domain (Emc, Id) function as negative regulators since they form heterodimers, but fail to bind DNA. The hairy-related proteins (hairy, E(spl), deadpan) also repress transcription although they can bind DNA. The proteins of this subfamily act together with co-repressor proteins, like groucho, through their C-terminal motif WRPW.

- The myc family of cellular oncogenes [4], which is currently known to contain four members: c-myc [E3], N-myc, L-myc, and B-myc. The myc genes are thought to play a role in cellular differentiation and proliferation.
- Proteins involved in myogenesis (the induction of muscle cells). In mammals MyoD1 (Myf-3), myogenin (Myf-4), Myf-5, and Myf-6 (Mrf4 or herculin), in birds CMD1 (QMF-1), in Xenopus MyoD and MF25, in Caenorhabditis elegans CeMyoD, and in Drosophila nautilus (nau).
- Vertebrate proteins that bind specific DNA sequences ('E boxes') in various immunoglobulin chains enhancers: E2A or ITF-1 (E12/pan-2 and E47/pan-1), ITF-2 (tcf4), TFE3, and TFEB.
- Vertebrate neurogenic differentiation factor 1 that acts as differentiation factor during neurogenesis.

- Vertebrate MAX protein, a transcription regulator that forms a sequence-specific DNA-binding protein complex with myc or mad.
- Vertebrate Max Interacting Protein 1 (MXI1 protein) which acts as a transcriptional repressor and may antagonize myc transcriptional activity by competing for max.
- Proteins of the bHLH/PAS superfamily which are transcriptional activators. In mammals, AH receptor nuclear translocator (ARNT), single-minded homologs (SIM1 and SIM2), hypoxia-inducible factor 1 alpha (HIF1A), AH receptor (AHR), neuronal pas domain proteins (NPAS1 and NPAS2), endothelial pas domain protein 1 (EPAS1), mouse ARNT2, and human BMAL1. In drosophila, single-minded (SIM), AH receptor nuclear translocator (ARNT), trachealess protein (TRH), and similar protein (SIMA).
- Mammalian transcription factors HES, which repress transcription by acting on two types of DNA sequences, the E box and the N box.
- Mammalian MAD protein (max dimerizer) which acts as transcriptional repressor and may antagonize myc transcriptional activity by competing for max.
- Mammalian Upstream Stimulatory Factor 1 and 2 (USF1 and USF2), which bind to a symmetrical DNA sequence that is found in a variety of viral and cellular promoters.
- Human lyl-1 protein; which is involved, by chromosomal translocation, in T-cell leukemia.
- Human transcription factor AP-4.
- Mouse helix-loop-helix proteins MATH-1 and MATH-2 which activate E box-dependent transcription in collaboration with E47.
- Mammalian stem cell protein (SCL) (also known as tal1), a protein which may play an important role in hemopoietic differentiation. SCL is involved, by chromosomal translocation, in stem-cell leukemia.
- Mammalian proteins Id1 to Id4 [5]. Id (inhibitor of DNA binding) proteins lack a basic DNA-binding domain but are able to form heterodimers with other HLH proteins, thereby inhibiting binding to DNA.
- Drosophila extra-macrochaetae (emc) protein, which participates in sensory organ patterning by antagonizing the neurogenic activity of the achaete-scute complex. Emc is the homolog of mammalian Id proteins.
- Human Sterol Regulatory Element Binding Protein 1 (SREBP-1), a transcriptional activator that binds to the sterol regulatory element 1 (SRE-1) found in the flanking region of the LDLR gene and in other genes.
- Drosophila achaete-scute (AS-C) complex proteins T3 (l'sc), T4 (scute), T5 (achaete) and T8 (asense). The AS-C proteins are involved in the determination of the neuronal precursors in the peripheral nervous system and the central nervous system.
- Mammalian homologs of achaete-scute proteins, the MASH-1 and MASH-2 proteins.

- Drosophila atonal protein (ato) which is involved in neurogenesis.
- Drosophila daughterless (da) protein, which is essential for neurogenesis and sex-determination.
- Drosophila deadpan (dpn), a hairy-like protein involved in the functional differentiation of neurons.
- Drosophila delilah (dei) protein, which is plays an important role in the differentiation of epidermal cells into muscle.
- Drosophila hairy (h) protein, a transcriptional repressor which regulates the embryonic segmentation and adult bristle patterning.
- Drosophila enhancer of split proteins E(spl), that are hairy-like proteins active during neurogenesis. also act as transcriptional repressors.
- Drosophila twist (twi) protein, which is involved in the establishment of germ layers in embryos.

- Maize anthocyanin regulatory proteins R-S and LC.

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 - Yeast centromere-binding protein 1 (CPF1 or CBF1). This protein is involved
   in chromosomal segregation.  It  binds  to a highly conserved DNA sequence,
   found in centromers and in several promoters.
 - Yeast INO2 and INO4 proteins.
 - Yeast  phosphate  system  positive  regulatory protein PHO4 which interacts
   with the upstream activating sequence of several acid phosphatase genes.
 - Yeast  serine-rich  protein  TYE7  that  is  required  for ty-mediated ADH2
   expression.
 - Neurospora crassa  nuc-1, a protein  that  activates  the  transcription of
   structural genes for phosphorus acquisition.
 - Fission yeast protein esc1 which  is involved in the sexual differentiation
   process.

The schematic representation of the helix-loop-helix domain is shown here:

    xxxxxxxxxxxxxxxxxxxxxxxx-------------------xxxxxxxxxxxxxxxxxxxxxx
      Amphipathic helix 1          Loop          Amphipathic helix 2

The profile  we  developed covers the helix-loop-helix dimerization domain and
the basic region.
```

Description of pattern(s) and/or profile(s)

Sequences known to belong to this class detected by the profile	ALL.
Other sequence(s) detected in Swiss-Prot	NONE.

Last update

August 2003 / Pattern removed.

References

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[E1]
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[E2]
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[E3]
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Database cross-reference

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Entries in Swiss-Prot and TrEMBL:

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	Entry name	AC	Gene names	Description	Organisms	Length
☐	AHR_HUMAN	P35869	**AHR**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Homo sapiens (Human)	848
☐	AHR_MOUSE	P30561	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Mus musculus (Mouse)	848
☐	AHR_MUSCR	Q8R4S7	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Mus caroli (Wild mouse) (Ricefield mouse)	854
☐	AHR_MUSMC	Q8R4S6	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Mus musculus castaneus (Southeastern Asian house mouse)	848
☐	AHR_MUSMM	Q8R4S5	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Mus musculus molossinus (Japanese house mouse)	883
☐	AHR_MUSSI	Q8R4S4	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah	Mus spicilegus (Steppe mouse)	854

				receptor) (AhR)		
☐	AHR_MUSSP	Q8R4S2	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Mus spretus (Western wild mouse)	854
☐	AHR_RABIT	O02747	**AHR**	**Ah receptor** (Aryl hydrocarbon receptor) (AhR)	Oryctolagus cuniculus (Rabbit)	847
☐	AHR_RAT	P41738	**Ahr**	**Aryl hydrocarbon receptor precursor** (Ah receptor) (AhR)	Rattus norvegicus (Rat)	853
☐	AMOS_DROME	Q9Y0A7	**amos**, Roi, rolo, *CG10393*	**Basic helix-loop-helix transcription factor Amos** (Reduced olfactory organs protein) (Rough eye protein) (Absent MD neurons and olfactory sensilla protein) (Amos protein)	Drosophila melanogaster (Fruit fly)	198
☐	ARLC_MAIZE	P13526	**LC**	**Anthocyanin regulatory Lc protein**	Zea mays (Maize)	610
☐	ARNT2_HUMAN	Q9HBZ2	**ARNT2**, KIAA0307	**Aryl hydrocarbon receptor nuclear translocator 2** (ARNT protein 2)	Homo sapiens (Human)	706
☐	ARNT2_MOUSE	Q61324	**Arnt2**	**Aryl hydrocarbon receptor nuclear translocator 2** (ARNT protein 2)	Mus musculus (Mouse)	712
				Aryl		

☐	ARNT_DROME	O15945	**tgo**, ARNT, HIF-1-BETA, *CG11987*	**hydrocarbon receptor nuclear translocator homolog** (dARNT) (Tango protein) (Hypoxia-inducible factor 1 beta)	Drosophila melanogaster (Fruit fly)	644
☐	ARNT_HUMAN	P27540	**ARNT**	**Aryl hydrocarbon receptor nuclear translocator** (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta) (HIF-1 beta)	Homo sapiens (Human)	789
☐	ARNT_MOUSE	P53762	**Arnt**	**Aryl hydrocarbon receptor nuclear translocator** (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta) (HIF-1 beta)	Mus musculus (Mouse)	791
☐	ARNT_RABIT	O02748	**ARNT**	**Aryl hydrocarbon receptor nuclear translocator** (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta) (HIF-1	Oryctolagus cuniculus (Rabbit)	790

				beta)		
☐	ARNT_RAT	P41739	**Arnt**	**Aryl hydrocarbon receptor nuclear translocator** (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta) (HIF-1 beta)	Rattus norvegicus (Rat)	800
☐	ARRS_MAIZE	P13027	**R-S**	**Anthocyanin regulatory R-S protein**	Zea mays (Maize)	612
☐	ASCL1_HUMAN	P50553	**ASCL1**, ASH1	**Achaete-scute homolog 1** (HASH1)	Homo sapiens (Human)	236
☐	ASCL1_MOUSE	Q02067	**Ascl1**, Ash1, Mash-1, Mash1	**Achaete-scute homolog 1** (Mash-1)	Mus musculus (Mouse)	231
☐	ASCL1_RAT	P19359	**Ascl1**, Ash1, Mash-1	**Achaete-scute homolog 1**	Rattus norvegicus (Rat)	233
☐	ASCL1_XENLA	Q06234	**ASCL1**, ASH1	**Achaete-scute homolog 1**	Xenopus laevis (African clawed frog)	199
☐	ASCL2_HUMAN	Q99929	**ASCL2**	**Achaete-scute homolog 2** (HASH2)	Homo sapiens (Human)	193
☐	ASCL2_MOUSE	O35885	**Ascl2**, Mash2	**Achaete-scute homolog 2** (Mash-2)	Mus musculus (Mouse)	263
☐	ASCL2_RAT	P19360	**Ascl2**, Ash2, Mash-2, Mash2	**Achaete-scute homolog 2**	Rattus norvegicus (Rat)	260
☐	ASCL3_HUMAN	Q9NQ33	**ASCL3**, SGN1	**Achaete-scute homolog 3** (bHLH transcriptional regulator Sgn-1)	Homo sapiens (Human)	180
☐	ASCL3_MOUSE	Q9JJR7	**Ascl3**, Mash3, Sgn1	**Achaete-scute homolog 3** (bHLH transcriptional regulator Sgn-1)	Mus musculus (Mouse)	174

				(Mash- 3)		
☐	AST3_DROME	P09774	**l(1)sc**, l'sc, T3, *CG3839*	**Achaete-scute complex protein T3** (Lethal of sc) (Lethal of scute protein)	Drosophila melanogaster (Fruit fly)	257
☐	AST4_DROME	P10084	**sc**, T4, *CG3827*	**Achaete-scute complex protein T4** (Scute protein)	Drosophila melanogaster (Fruit fly)	345
☐	AST5_DROME	P10083	**ac**, T5, *CG3796*	**Achaete-scute complex protein T5** (Achaete)	Drosophila melanogaster (Fruit fly)	201
☐	AST8_DROME	P09775	**ase**, T8, *CG3258*	**Achaete-scute complex protein T8** (Asense)	Drosophila melanogaster (Fruit fly)	486
☐	ATOH1_HUMAN	Q92858	**ATOH1**, ATH1	**Atonal protein homolog 1** (Helix-loop-helix protein hATH-1)	Homo sapiens (Human)	354
☐	ATOH1_MOUSE	P48985	**Atoh1**, Ath1	**Atonal protein homolog 1** (Helix-loop-helix protein mATH-1) (MATH1)	Mus musculus (Mouse)	351
☐	ATOH1_PANTR	Q5IS79	**ATOH1**	**Atonal protein homolog 1**	Pan troglodytes (Chimpanzee)	356
☐	ATO_DROME	P48987	**ato**, *CG7508*	**Atonal protein**	Drosophila melanogaster (Fruit fly)	312
☐	BETA3_MESAU	O09029		**BETA3 protein**	Mesocricetus auratus (Golden hamster)	367
☐	BHLH2_HUMAN	O14503	**BHLHB2**, DEC1, SHARP2,	**Class B basic helix-loop-helix protein 2** (bHLHB2) (Differentially expressed in chondrocytes protein 1)	Homo sapiens (Human)	412

			STRA13	(DEC1) (Enhancer-of-split and hairy-related protein 2) (SHARP-2) (Stimulated with retinoic acid 13)		
☐	BHLH2_MOUSE	O35185	**Bhlhb2**, Clast5, Stra13	**Class B basic helix-loop-helix protein 2** (bHLHB2) (Stimulated with retinoic acid 13) (E47 interaction protein 1) (eipl)	Mus musculus (Mouse)	411
☐	BHLH2_RAT	O35780	**Bhlhb2**, Sharp2	**Class B basic helix-loop-helix protein 2** (bHLHB2) (Enhancer-of-split and hairy-related protein 2) (SHARP-2)	Rattus norvegicus (Rat)	411
☐	BHLH3_HUMAN	Q9C0J9	**BHLHB3**, DEC2, SHARP1	**Class B basic helix-loop-helix protein 3** (bHLHB3) (Differentially expressed in chondrocytes protein 2) (hDEC2) (Enhancer-of-split and hairy-related protein 1) (SHARP-1)	Homo sapiens (Human)	482
☐	BHLH3_MOUSE	Q99PV5	**Bhlhb3**, Dec2	**Class B basic helix-loop-helix protein 3** (bHLHB3) (Differentially expressed in chondrocytes protein 2) (mDEC2)	Mus musculus (Mouse)	410
				Class B basic helix-loop-helix protein 3		

☐	BHLH3_RAT	O35779	**Bhlhb3**, Sharp1	(bHLHB3) (Enhancer-of-split and hairy-related protein 1) (SHARP-1)	Rattus norvegicus (Rat)	410
☐	BIM1_ARATH	Q9LEZ3	**BIM1**, EN126, *At5g08130*, *T22D6.70*	**Transcription factor BIM1** (BES1-interacting Myc-like protein 1) (Transcription factor EN 126) (AtbHLH 46)	Arabidopsis thaliana (Mouse-ear cress)	530
☐	BIM2_ARATH	Q9CAA4	**BIM2**, EN125, *At1g69010*, *T6L1.19*	**Putative transcription factor BIM2** (BES1-interacting Myc-like protein 2) (Transcription factor EN 125) (AtbHLH 102)	Arabidopsis thaliana (Mouse-ear cress)	311
☐	BIM3_ARATH	Q9FMB6	**BIM3**, EN127, *At5g38860*, *K15E6.7*, *K15E6.40*	**Putative transcription factor BIM3** (BES1-interacting Myc-like protein 3) (Transcription factor EN 127) (AtbHLH 141)	Arabidopsis thaliana (Mouse-ear cress)	298
☐	BMAL1_HUMAN	O00327	**ARNTL**, BMAL1, MOP3	**Aryl hydrocarbon receptor nuclear translocator-like protein 1** (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (Basic-helix-loop- helix-PAS orphan MOP3) (bHLH-PAS protein JAP3)	Homo sapiens (Human)	626
				Aryl hydrocarbon		

☐	BMAL1_MESAU	O88529	**ARNTL**, BMAL1	**receptor nuclear translocator-like protein 1** (Brain and muscle ARNT-like 1)	Mesocricetus auratus (Golden hamster)	626
☐	BMAL1_MOUSE	Q9WTL8	**Arntl**, Bmal1	**Aryl hydrocarbon receptor nuclear translocator-like protein 1** (Brain and muscle ARNT-like 1) (Arnt3)	Mus musculus (Mouse)	632
☐	BMAL1_RAT	Q9EPW1	**Arntl**, Bmal1, Tic	**Aryl hydrocarbon receptor nuclear translocator-like protein 1** (Brain and muscle ARNT-like 1) (Tic)	Rattus norvegicus (Rat)	626
☐	CBF1_KLULA	P49379	**CBF1**, CPF1, *KLLA0B13761g*	**Centromere-binding protein 1** (CBP-1) (Centromere-binding factor 1) (Centromere promoter factor 1)	Kluyveromyces lactis (Yeast)	359
☐	CBF1_YEAST	P17106	**CBF1**, CEP1, CP1, CPF1, *YJR060W*, *J1730*	**Centromere-binding protein 1** (CBP-1) (Centromere-binding factor 1) (Centromere promoter factor 1)	Saccharomyces cerevisiae (Baker's yeast)	351
☐	CLOCK_DROME	O61735	**Clk**, CLOCK, jrk, PAS1, *CG7391*	**Circadian locomoter output cycles Kaput protein** (dCLOCK) (dPAS1)	Drosophila melanogaster (Fruit fly)	1027

☐	CLOCK_HUMAN	O15516	**CLOCK**, KIAA0334	**Circadian locomoter output cycles kaput protein** (hCLOCK)	Homo sapiens (Human)	846
☐	CLOCK_MOUSE	O08785	**Clock**	**Circadian locomoter output cycles kaput protein** (mCLOCK)	Mus musculus (Mouse)	855
☐	CYCL_DROME	O61734	**cyc**, *CG8727*	**Cycle protein** (Brain and muscle ARNT-like 1) (BMAL1) (MOP3)	Drosophila melanogaster (Fruit fly)	413
☐	DA_DROME	P11420	**da**, *CG5102*	**Daughterless protein**	Drosophila melanogaster (Fruit fly)	710
☐	DEI_DROME	P41894	**dei**, *CG5441*	**Helix-loop-helix protein delilah**	Drosophila melanogaster (Fruit fly)	360
☐	DPN_DROME	Q26263	**dpn**, *CG8704*	**Deadpan protein**	Drosophila melanogaster (Fruit fly)	435
☐	EGL1_ARATH	Q9CAD0	**BHLH002**, BHLH2, EGL1, MYC146, *At1g63650*, *F24D7.16*	**Transcription factor EGL1** (ENHANCER OF GLABRA3) (Basic helix-loop- helix protein 2) (bHLH2) (AtbHLH002) (AtMyc-146)	Arabidopsis thaliana (Mouse-ear cress)	596
☐	EMC_DROME	P18491	**emc**, *CG1007*	**Extra-macrochaetae protein**	Drosophila melanogaster (Fruit fly)	199
☐	EPAS1_HUMAN	Q99814	**EPAS1**, HIF2A	**Endothelial PAS domain protein 1** (EPAS-1) (Member of PAS protein 2) (MOP2) (Hypoxia-	Homo sapiens (Human)	870

				inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (HLF)		
☐	EPAS1_MOUSE	P97481	**Epas1**, Hif2a	**Endothelial PAS domain protein 1** (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (MHLF) (HIF-related factor) (HRF)	Mus musculus (Mouse)	874
☐	EPAS1_RAT	Q9JHS1	**Epas1**, Hif2a	**Endothelial PAS domain protein 1** (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)	Rattus norvegicus (Rat)	874
☐	ESC1_SCHPO	Q04635	**esc1**, *SPAC56F8.16*	**Protein esc1**	Schizosaccharomyces pombe (Fission yeast)	413
☐	ESM3_DROME	Q01068	**HLHm3**, *CG8346*	**Enhancer of split m3 protein** (E(spl)m3) (HLH-m3)	Drosophila melanogaster (Fruit fly)	224
☐	ESM5_DROME	P13096	**HLHm5**, *CG6096*	**Enhancer of split m5 protein** (E(spl)m5)	Drosophila melanogaster (Fruit fly)	178
☐	ESM7_DROME	P13097	**HLHm7**, *CG8361*	**Enhancer of split m7 protein** (E(spl)m7)	Drosophila melanogaster (Fruit fly)	186
☐	ESM8_DROHY	Q07291	**E(spl)**, M8	**Enhancer of split m8 protein** (E(spl)m8)	Drosophila hydei (Fruit fly)	183
☐	ESM8_DROME	P13098	**E(spl)**, m8, *CG8365*	**Enhancer of split m8 protein**	Drosophila melanogaster (Fruit	179

				(E(spl)m8)	fly)	
☐	ESMB_DROME	Q01069	**HLHm-beta,** *CG14548*	**Enhancer of split mbeta protein** (E(spl) mbeta) (HLH-mbeta) (Split locus enhancer protein mA)	Drosophila melanogaster (Fruit fly)	195
☐	ESMC_DROME	Q01070	**HLHm-gamma,** *CG8333*	**Enhancer of split mgamma protein** (E(spl) mgamma) (HLH-mgamma) (Split locus enhancer protein mB)	Drosophila melanogaster (Fruit fly)	205
☐	ESMD_DROME	Q01071	**HLHm-delta,** *CG8328*	**Enhancer of split mdelta protein** (E(spl) mdelta) (HLH-mdelta) (Split locus enhancer protein mC)	Drosophila melanogaster (Fruit fly)	173
☐	FIGLA_HUMAN	Q6QHK4	**FIGLA**	**Factor in the germline alpha** (Transcription factor FIGa) (FIGalpha)	Homo sapiens (Human)	219
☐	FIGLA_MOUSE	O55208	**Figla**	**Factor in the germline alpha** (Transcription factor FIGa) (FIGalpha)	Mus musculus (Mouse)	194
☐	HAIR_DROME	P14003	**h,** *CG6494*	**Hairy protein**	Drosophila melanogaster (Fruit fly)	337
☐	HAIR_DROVI	P29303	**h**	**Hairy protein**	Drosophila virilis (Fruit fly)	378
☐	HAND1_CHICK	Q90691	**HAND1,** EHAND	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic	Gallus gallus (Chicken)	202

				nervous sytem and neural crest derivatives-expressed protein 1) (eHAND)		
☐	HAND1_HUMAN	O96004	**HAND1**, EHAND	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-expressed protein 1) (eHAND)	Homo sapiens (Human)	215
☐	HAND1_MOUSE	Q64279	**Hand1**, Ehand, Hxt, Thing1	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-expressed protein 1) (eHAND) (Helix-loop-helix transcription factor expressed in extraembryonic mesoderm and trophoblast) (Thing-1) (Th1)	Mus musculus (Mouse)	216
				Heart- and neural crest derivatives-expressed protein 1		

☐	HAND1_RABIT	P57100	**HAND1**, EHAND	(Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-expressed protein 1) (eHAND)	Oryctolagus cuniculus (Rabbit)	215
☐	HAND1_RAT	P97832	**Hand1**, Ehand	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-expressed protein 1) (eHAND)	Rattus norvegicus (Rat)	216
☐	HAND1_SHEEP	Q28555	**HAND1**, EHAND, HXT	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-expressed protein 1) (eHAND)	Ovis aries (Sheep)	204
☐	HAND1_XENLA	O73615	**HAND1**, EHAND	**Heart- and neural crest derivatives-expressed protein 1** (Extraembryonic tissues, heart, autonomic nervous sytem and neural crest derivatives-	Xenopus laevis (African clawed frog)	197

				expressed protein 1) (eHAND)		
☐	HAND2_BRARE	P57102	**hand2**, dhand	**Heart- and neural crest derivatives-expressed protein 2** (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND)	Brachydanio rerio (Zebrafish) (Danio rerio)	208
☐	HAND2_CHICK	Q90690	**HAND2**, DHAND	**Heart- and neural crest derivatives-expressed protein 2** (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND)	Gallus gallus (Chicken)	216
☐	HAND2_HUMAN	P61296	**HAND2**, DHAND	**Heart- and neural crest derivatives-expressed protein 2** (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND)	Homo sapiens (Human)	217
				Heart- and neural crest derivatives-expressed protein 2 (Deciduum,		

☐	HAND2_MOUSE	Q61039	**Hand2**, Dhand, Hed, Thing2	heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND) (Helix-loop-helix transcription factor expressed in embryo and deciduum) (Thing-2)	Mus musculus (Mouse)	217
☐	HAND2_RAT	P61295	**Hand2**, Dhand	**Heart- and neural crest derivatives-expressed protein 2** (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND)	Rattus norvegicus (Rat)	217
☐	HAND2_XENLA	P57101	**HAND2**, DHAND	**Heart- and neural crest derivatives-expressed protein 2** (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND)	Xenopus laevis (African clawed frog)	210
☐	HEN1_HUMAN	Q02575	**NHLH1**, HEN1	**Helix-loop-helix protein 1** (HEN1) (Nescient helix loop helix 1) (NSCL- 1)	Homo sapiens (Human)	133
				Helix-loop-helix protein 1		

☐	HEN1_MOUSE	Q02576	**Nhlh1**, Hen1	(HEN1) (Nescient helix loop helix 1) (NSCL- 1)	Mus musculus (Mouse)	133
☐	HEN2_HUMAN	Q02577	**NHLH2**, HEN2	**Helix-loop-helix protein 2** (HEN2) (Nescient helix loop helix 2) (NSCL- 2)	Homo sapiens (Human)	135
☐	HEN2_MOUSE	Q64221	**Nhlh2**, Hen2	**Helix-loop-helix protein 2** (HEN2) (Nescient helix loop helix 2) (NSCL- 2)	Mus musculus (Mouse)	135
☐	HES1_CHICK	O57337	**HES1**, HAIRY1	**Transcription factor HES-1** (C-HAIRY1)	Gallus gallus (Chicken)	290
☐	HES1_HUMAN	Q14469	**HES1**, HL, HRY	**Transcription factor HES-1** (Hairy and enhancer of split 1) (Hairy- like) (HHL) (Hairy homolog)	Homo sapiens (Human)	280
☐	HES1_MOUSE	P35428	**Hes1**, Hes-1	**Transcription factor HES-1** (Hairy and enhancer of split 1)	Mus musculus (Mouse)	282
☐	HES1_RAT	Q04666	**Hes1**, Hes-1, Hl	**Transcription factor HES-1** (Hairy and enhancer of split 1) (Hairy- like) (RHL)	Rattus norvegicus (Rat)	281
☐	HES2_HUMAN	Q9Y543	**HES2**	**Transcription factor HES-2** (Hairy and enhancer of split 2)	Homo sapiens (Human)	173
☐	HES2_MOUSE	O54792	**Hes2**	**Transcription factor HES-2** (Hairy and enhancer of split	Mus musculus (Mouse)	157

				2)			

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